

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Previously Amended) A primer which amplifies *groEL2* gene fragment of at least one *Streptomyces* species consisting of the nucleotide sequence of SEQ ID NO: 1.

2. (Currently Amended) A primer which amplifies *groEL2* gene fragment of at least one *Streptomyces* species consisting of the nucleotide sequence of SEQ ID NO: 2 and ~~optionally additional nucleotide sequences comprising the complement of adjacent nucleotide sequences of *S. lividans* (GenBank No. X95971), *S. albus* (GenBank No. M76658), and *T. paurometabola* (GenBank No. AF352578).~~

3. (Withdrawn) A *groEL2* gene fragment derived from *Streptomyces* species or fragment thereof comprising a polynucleotide chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.

4. (Currently Amended) An isolated *groEL2* gene fragment derived from *S. scabiei* ~~a potato scab pathogenic microorganism~~ comprising SEQ ID NO: 43.

5. (Withdrawn) A method for identifying *Streptomyces* species comprising:

- a) amplifying *groEL2* gene fragment of target strain using a primer which is capable of specifically amplifying *groEL2* gene of *Streptomyces* species;
- b) analyzing the nucleotide sequence of *groEL2* gene fragment thus amplified;

and

c) comparing the nucleotide sequence obtained in b) with that of *groEL2* gene fragment of a reference strain.

6. (Withdrawn) The method of claim 5, wherein the primer is chosen from at least one of

a) a primer comprising the nucleotide sequence of SEQ ID NO: 1 and

b) a primer comprising the nucleotide sequence of SEQ ID NO: 2.

7. (Withdrawn) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.

8. (Withdrawn) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is chosen from the nucleotide sequences of SEQ ID NOs: 43 to 61.

9. (Withdrawn) The method of claim 5, wherein c) further comprises multi-aligning the nucleotide sequences and forming a phylogenetic tree.

10. (Currently Amended) A primer which specifically amplifies *groEL2* gene fragment of at least one *Streptomyces* species consisting essentially of the nucleotide sequence of SEQ ID NO: 2.

11. (Cancelled)

12. (Previously Presented) The *groEL2* gene fragment of claim 4, wherein the fragment is SEQ ID NO: 43.

13. (Withdrawn) An isolated *groEL2* gene fragment derived from a potato scab pathogenic microorganism comprising a polynucleotide chosen from the nucleotide sequences of any one of SEQ ID NOs: 44 to 61.

14. (Currently Amended) An isolated *groEL2* gene fragment produced by amplification from a ~~potato scab pathogenic~~ microorganism using

a) a primer consisting of the nucleotide sequence of SEQ ID NO: 1 and

b) a primer consisting of the nucleotide sequence of SEQ ID NO: 2,

wherein said microorganism is chosen from *R. equi*, *S. acrimycini*, *S. aculeolatus*, *S. alanosinicus*, *S. albireticuli*, *S. albofaciens*, *S. albogriseolus*, *S. alboniger*, *S. albus*, *S. ambofaciens*, *S. aminophilus*, *S. anandii*, *S. argenteolus*, *S. bambergiensis*, *S. capillispiralis*, *S. carpinesis*, *S. catenulae*, *S. cellulosa*, *S. chartreusis*, *S. chattanoogensis*, *S. cinereoruber*, *S. cinnamomensis*, *S. cirratus*, *S. coeruleorubidus*, *S. collinus*, *S. corchorusii*, *S. diastaticus*, *S. djakartensis*, *S. erumpens*, *S. fulvissimus*, *S. galilaeus*, *S. griseochromogenes*, *S. griseolus*, *S. griseoviridis*, *S. humiferus*, *S. hygrosopicus*, *S. hygrosopicus*, *S. minutiscleroticus*, *S. murinus*, *S. nodosus*, *T. paurometabola*, *S. acidiscabies*, *S. bottropensis*, *S. disastatochromogenes*, *S. neyagawaensis*, *S. scabiei*, and *S. turgidiscabies*.